

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 05-28-03
Searcher: Beverly E 4994
Terminal time: 20
Elapsed time: _____
CPU time: _____
Total time: 23
Number of Searches: _____
Number of Databases: 1

Search Site

_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG Suite
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
_____ Other CGN

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 08:37:43 ; Search time 6628 seconds

(Without alignments)
11086.992 Million cell updates/sec

Title: US-09-993-731-10

Sequence: 1 cctcggtcgtgcgtgccc.....cgatctctctccacaga 2525

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

rd size : 100

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : GenEmbl:*
1: gb_da:*
2: gb_hcg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_mu:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sy:*
28: em_un:*
29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_rtd:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_sy:*
39: em_hgtgo_hum:*
40: em_hgtgo_mus:*
41: em_hgtgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1549	61.3	4501	9	BC008782	BC008782 Homo sapi
2	820	32.5	7543	9	HS8242601	AJ242601 Homo sapi
3	400	15.8	191078	2	AC022505	AC022505 Homo sapi
4	340	13.5	1813	9	HS016258	U16258 Human 1 kap
5	138	5.5	69215	2	AC087337	AC087337 Homo sapi

ALIGNMENTS

RESULT 1
BC008782
LOCUS
DEFINITION
BC008782 4501 bp mRNA linear PRI 12-JUL-2001
Homo sapiens, nuclear factor of kappa light polypeptide gene
enhancer in B-cells inhibitor-like 2, clone MGC:3398 IMAGE:3628374,
mRNA, complete cds.
ACCESSION
BC008782.1 GI:14250635
VERSION
BC008782.1
KEYWORDS
MGC.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 4501)
JOURNAL
Submitted (25-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgabs-ref@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nigri.nih.gov
Shvchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, Q.L., Mastello, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantrop, S., Thomas, P.J.,
Tiongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILM at: <http://image.llnl.gov>
Series: IRAL Plate: 12 Row: C Column: 8
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 7305310.
Location/Qualifiers

FEATURES

1. 4501
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="MGC:3398 IMAGE:3628374"
/tissue="Brain, neuroblastoma"
/clone_lib="NIH_MGC_19"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
474. .4133

Prod. No. is the number of results predicted by chance to have a

CDS

```
/codon_start=1
/product="nuclear factor of kappa light polypeptide gene
enhancer in B-cells inhibitor-like 2"
/protein_id="AA08782.1"
/db_xref="gi:14250636"
/translation="MTRRLYLNGITRESIQATLNDPFRKSLFLEONHLYEDLER
ARVNLGTHMRAGHDSQMRKLEBARCATMTRKRWESCCVIAQVLDLDDLELAA
KRALKAVRLRSQKPYORAAICQMLQVNLVAVLQGLEAREDDPGAMVLEIOLGD
LESAQGPRAAEAYOKORFAPLAEEDRPAERAIIIVSLATLGDMDHGAVERHE
ELRLTSQVLEAEATWLNIALSREAGDAVELAPFOALSCAOQARPOQVLOVLO
HLRLVQLRPOEAPETRELRLEVEDEEEAEAEAAETSEALPAGVEYLESEG
EDDIDGLPOLDEDELOGLHGRKRSKMRNMDMETILLHRCITGOLRQVLDVRO
GHLNPDYQSWPLPHEACNVKGLFVRLRRMDADVDGCGGCGCTPIRLDALNG
HEVVALLEBKASVTLRTRKSLSPETLQWKTIRBDLDETROKAMEMLDQAA
ASGDPHSSQAFHTPSLTPDETSPPLSCPPSSNSTPLPASVHNRVSPQAAAP
AMARPKSRHGPASSSSSEDSAGAPRSQKPRCSATNOVAAWMTGPPASNRAEA
TASTSRAAYQAIIRVGSQSRIGLPGPRHSAKALPQOALIPEEELGDMLELMD
LTRRRPRPRGTDNRPRSSSTSGDSESRPARAKOVRTCMQSCSAVYNAQPSIA
SEPPSPSTPRVSEPSDSSAAGOPLPAPPPPIRVAYOVQDHLFLIPVHSDYSA
AMLEOAAORYOTCGLLPRULRKEGALLAPDILPDVLOSDEVLAVETSMDLPL
TDRYRACOSISGEGHOVALVEPLSGISGSCSLADQOALTPLELRLKLTHTLR
ELRLAGNRLOKCYAEVLAELGTPSLALDLSSNHLGREGQLMGLPQATLOSL
BELDLSNMPJEDGGSJASLHACPLSTLRLOCGFGSEFLSHQTLVGSFADAE
HLKTLISYNAHLGAPALARLQSLPAGTLLHLELSVAAKGDSIDMEVFXLAKG
CALAHLTLSANHLGDKAVRDICLSLPSLISLIDISANPEISCSLIEELITLQRP
OGLSFLGSGCAVGGPLGLQIMDKIAQLRELOCSRLCAEDRDALROLQPSRPGG
ECTLDHSGKLEFFRL"
```

BASE COUNT 877 a 1496 c 1437 g 691 t

Query Match	Best Local Similarity	Score	DB 9	Length	4501
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	99.8%	1549			

Query 633 CAGCACACACCACTACTAGAGTGGACATTCCTCGCCACACACAGAGAGCTCAG 692
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 258 CAGCACACACCACTACTAGAGTGGACATTCCTCGCCACACACAGAGAGCTCAG 317

QY 693 AGGCGCTGGGCCACCATGGCGCCGACCCACCTGACATCTATGACCACTGCGAGT 752
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 318 AGGCGCTGGGCCACCATGGCGCCGACCCACCTGACATCTATGACCACTGCGAGT 377

QY 753 GATGCTTGTGACAGGAGCTGCTTGTGAGAGAGCTTGTGATTTGTGATGAGAG 812
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 378 GATGCTTGTGACAGGAGCTGCTTGTGAGAGAGCTTGTGATTTGTGATGAGAG 437

QY 813 TTGGAGGGGACACTGCGCCAGGAGAGCTGATGATGAGAGAGAGAGAGAGAGAG 872
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 438 CTGGAGGGGACACTGCGCCAGGAGAGCTGATGATGAGAGAGAGAGAGAGAGAG 497

QY 873 CTGGAGCTTACCTTTGAGAGCTTGACAGACAGCCCTGTCAGACGATTTACTTCAGAG 932
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 498 CTGGAGCTTACCTTTGAGAGCTTGACAGACAGCCCTGTCAGACGATTTACTTCAGAG 557

QY 933 AGCATCTTCTTGGGAGGACAGACACCTTTACAGAGAGACCTATTCCGCGCCGTACAC 992
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 558 AGCATCTTCTTGGGAGGACAGACACCTTTACAGAGAGACCTATTCCGCGCCGTACAC 617

QY 993 CTGGGACACCATCACTGGCGGCGGAGGAGCACTCCAGGCTATGCGCTTGTGAGAGGT 1052
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 618 CTGGGACACCATCACTGGCGGCGGAGGAGCACTCCAGGCTATGCGCTTGTGAGAGGT 677

QY 1053 GCCCGGAGGTGTGGACACACATGAGAGAGGCTTTCATGAGAGAGAGAGAGAGAG 1112
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 678 GCCCGGAGGTGTGGACACACATGAGAGAGGCTTTCATGAGAGAGAGAGAGAGAG 737

QY 1113 ATTGACAGAGTCTTCAAGAGACCTGGAGAGATTTTGGTGCCAGAGAGAGAGAGAG 1172
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 738 ATTGACAGAGTCTTCAAGAGACCTGGAGAGATTTTGGTGCCAGAGAGAGAGAGAG 797

QY 1173 GCTTACAGAGGTGCTCCAGAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1232
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 798 GCTTACAGAGGTGCTCCAGAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 857

QY 1233 CATGTGCTGGCAGTGTGCTCCGCTGACAGACAGCTGGAAGAGGTGAGGGCAGACAGCTT 1292
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 856 CATGTGCTGGCAGTGTGCTCCGCTGACAGACAGCTGGAAGAGGTGAGGGCAGACAGCTT 917

QY 1293 CAGGCTGCGCATGTGATCTGTGAGCAGCTAGGGAGCTTCTTCCAAAGCAGAGAGACTTTT 1352
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 918 CAGGCTGCGCATGTGATCTGTGAGCAGCTAGGGAGCTTCTTCCAAAGCAGAGAGACTTTT 977

QY 1353 CCCAGGAGAGCTGAGAGGCTTACAGAGAGAGCTGCTTTTCTGAGAGCTGTCAGACAGCG 1412
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 978 CCCAGGAGAGCTGAGAGGCTTACAGAGAGAGCTGCTTTTCTGAGAGCTGTCAGACAGCG 1037

QY 1413 GGTGCTGAGCGCGCCATCATCTACAGCTGCTCCGTGCGCACACACTGGAGAGATGAAGAG 1472
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1038 GGTGCTGAGCGCGCCATCATCTACAGCTGCTCCGTGCGCACACACTGGAGAGATGAAGAG 1097

QY 1473 CACCATGAGGAGCGCGCCATCATCTACAGCTGCTCCGTGCGCACACACTGGAGAGATGAAGAG 1532
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1098 CACCATGAGGAGCGCGCCATCATCTACAGCTGCTCCGTGCGCACACACTGGAGAGATGAAGAG 1157

QY 1533 GAGGAGGCGCAAGACTGCTGACATTGACATGTCCCGGAGAGAGCGCGCGATGCTTAC 1592
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1158 GAGGAGGCGCAAGACTGCTGACATTGACATGTCCCGGAGAGAGCGCGCGATGCTTAC 1217

QY 1593 GAGCTGCTGGCGCGCGCTGCTTCCAGAAAGCGCTGAGCTGTGCTGAGAGAGCGCGCTGCG 1652
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1218 GAGCTGCTGGCGCGCGCTGCTTCCAGAAAGCGCTGAGCTGTGCTGAGAGAGCGCGCTGCG 1277

QY 1653 CAGCTGCAAGAGAGAGCTTGTGACATCTCCATACCGTGAGCTGAGCTGACAGCCCGAG 1712
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1278 CAGCTGCAAGAGAGAGCTTGTGACATCTCCATACCGTGAGCTGAGCTGAGCTGAGCCCGAG 1337

QY 1713 GAGCGCCCTGAGACCGAAACAGAGCTGCGGAGCTGCTGATCTGAAGTGAAGTGAAG 1772
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1338 GAGCGCCCTGAGACCGAAACAGAGCTGCGGAGCTGCTGATCTGAAGTGAAGTGAAG 1397

QY 1773 CAGGAGAGAGCGGAGAGAGCGCGGACCCACAGCGGAGAGAGAGAGAGAGAGAGAG 1832
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1398 GAGGAGAGAGCGGAGAGAGCGCGGACCCACAGCGGAGAGAGAGAGAGAGAGAGAG 1457

QY 1833 GTGAGCTTCTCAG 1892
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1458 GTGAGCTTCTCAG 1517

QY 1893 GAGGAGCTTCAAGGCGCACCTGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1952
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1518 GAGGAGCTTCAAGGCGCACCTGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1577

QY 1953 ATGGGAG 2012
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1578 ATGGGAG 1637

QY 2013 CTGTGAG 2072
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1638 CTGTGAG 1697

QY 2073 GAGGCTTCAAGCTACGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2132
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1698 GAGGCTTCAAGCTACGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1757

QY 2133 GTGAG 2192
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1758 GTGAG 1817

QY 2193 GTGAG 2252
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1818 GTGAG 1877

QY 2253 ACTGGAAG 2312
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1878 ACTGGAAG 1937

QY 2313 GACCTGACCTGAGACGCGGACAGAGCCAGGCGCATGTGAGATGCTCTCCAGCGGCT 2372
|||||
Db 1938 GACCTGACCTGAGACGCGGACAGAGCCAGGCGCATGTGAGATGCTCTCCAGCGGCT 1997
QY 2373 GCCTGCGGCGCCAG 2385
|||||
Db 1998 GCCTGCGGCGCCAG 2010

RESULT 2
LOCUS HSA249601 7543 bp DNA linear PRI 07-SEP-2000
DEFINITION Homo sapiens partial NFKBIL2 gene for IkappaB, exons 1-13.
ACCESSION AJ249601
VERSION AJ249601.1 GI:6580427
KEYWORDS IkappaB; NFKBIL2 gene.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 7543)
AUTHORS Norman,D.A. and Barton,P.J.
TITLE Isolation, sequence, and chromosomal localisation of the human
IkappaB gene (NFKBIL2)
JOURNAL Ann. Hum. Genet. 64 (Pt 1), 15-23 (2000)
MEDLINE 21141789
PUBMED 11246458
REFERENCE 2 (bases 1 to 7543)
AUTHORS Norman,D.A.M.
TITLE Direct Submission
JOURNAL Submitted (14-SEP-1999) Norman D.A.M., Cardiothoracic Surgery,
National Heart and Lung Institute, Dovehouse Street, London, SW3
6LY, UNITED KINGDOM

FEATURES
source
location/Qualifiers
1..7543
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
/clone_lib="RPC11"
1..7543
/gene="NFKBIL2"
join(<1..819,1151..1280,1545..1716,1806..1920,2847..2992,
3088..3240,3482..3607,3748..3937,5222..5304,5399..5488,
6862..6934,7041..7204,7280..>7543)
/gene="NFKBIL2"
<1..819
/gene="NFKBIL2"
/number=1
820..1150
/gene="NFKBIL2"
/number=1
1151..1280
/gene="NFKBIL2"
/number=2
join(1180..1280,1545..1716,1806..1920,2847..2992,
3088..3240,3482..3607,3748..3937,5222..5304,5399..5488,
6862..6934,7041..7204,7280..>7543)
/gene="NFKBIL2"
/function="unknown"
/codon_start=1
/product="IkappaB"
/protein_id="CA63467.1"
/db_xref="GI:6580428"
/db_xref="SPRREBL:Q9UGJ2"
/translation="MKRLYLNLGLTFESLQOTALCNDYFRKSTPLAEQNHLYEDLR
ARYNLGTIMHRAQSHOAMKCLEGARECAHTMKRMESECCVIAQVLODIDELDA
KRAIKAYRISGSKPYQRAAICQNLQHVLAAYVRLQQLLEAGRDPQAGMVICEDLD
LFSKADPRAAAYOKOLRFAELLDRPAERAIIHVSLATYLGDKDHGAGVRHYEE
ELRSGNVLEAKTWLNTALSRSEAGDAYELLAPCFOKALSCAQQAQAOAQLQROYLO
HHTVQLRLQPOEAPEETETRELTSVAEDEDEEAEAEAAALAESEALAEAGEVLES
EDDTGELTQLEDEDELQGLGRKRSKNNRRNDKCEYLIHACIGSLGRVODIIVRO
GHLNPRDYCGWTPLEHACNYGHLTVRFLLDGAADVDPGGCGITPLDLALNG

HEPVALLEKRGASVTLTRKGLSPLETLQOMVKLYRRDLDETROKARAMEMLLOAA
ASGQKQGVPCPCWGCATAAESPRALISDASQYEREVPGCLMTHSLSHR"
intron
1281..1544
/gene="NFKBIL2"
/number=2
1545..1716
/gene="NFKBIL2"
/number=3
1717..1805
/gene="NFKBIL2"
/number=3
1806..1920
/gene="NFKBIL2"
/number=4
1921..2846
/gene="NFKBIL2"
/number=4
2847..2992
/gene="NFKBIL2"
/number=5
2993..3087
/gene="NFKBIL2"
/number=5
3088..3240
/gene="NFKBIL2"
/number=6
3241..3481
/gene="NFKBIL2"
/number=6
3482..3607
/gene="NFKBIL2"
/number=7
3608..3747
/gene="NFKBIL2"
/number=7
3748..3937
/gene="NFKBIL2"
/number=8
3938..5221
/gene="NFKBIL2"
/number=8
5222..5304
/gene="NFKBIL2"
/number=9
5305..5398
/gene="NFKBIL2"
/number=9
5399..5488
/gene="NFKBIL2"
/number=10
5489..6861
/gene="NFKBIL2"
/number=10
6862..6934
/gene="NFKBIL2"
/number=11
6935..7040
/gene="NFKBIL2"
/number=11
7041..7204
/gene="NFKBIL2"
/number=12
7205..7279
/gene="NFKBIL2"
/number=12
7280..>7543
/gene="NFKBIL2"
/number=13

BASE COUNT 1407 a 2143 c 2547 g 1445 t 1 others
ORIGIN
Query Match 32.5%; Score 820; DB 9; Length 7543;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 820; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 CTTGGGCTGTGGCGTGGCCACCAAGATGAGAGGCGCCGCGGAGATGAGAGT 60
    |||||
Db 1 CTCGGGCTGTGGCGTGGCCACCAAGATGAGAGGCGCCGCGGAGATGAGAGT 60
OY 61 ACCGGCTGTGGAGTGGCGGCGCCCTACTGCGCTGCTCCAGCCGCGTCCCTG 120
    |||||
Db 61 ACCGGCTGTGGAGTGGCGGCGCCCTACTGCGCTGCTCCAGCCGCGTCCCTG 120
OY 121 GAGCCCTTTCTAGAGAGGAGGAGCTGCTGCTGCTGCTGAGAGGAGGAGG 180
    |||||
Db 121 GAGCCCTTTCTAGAGAGGAGGAGCTGCTGCTGCTGCTGAGAGGAGGAGG 180
OY 181 ACACCTTACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
    |||||
Db 181 ACACCTTACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
OY 241 ACAGCCTTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
    |||||
Db 241 ACAGCCTTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
OY 301 CGTATTATTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
    |||||
Db 301 CGTATTATTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
OY 361 ACCCTGCTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
    |||||
Db 361 ACCCTGCTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
OY 421 CGTGACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
    |||||
Db 421 CGTGACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
OY 481 GAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
    |||||
Db 481 GAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
OY 541 CTTTCTTACCAAGACAGAGGCTCTGTGGAGATCTGGCGGTTGCTTGTGAG 600
    |||||
Db 541 CTTTCTTACCAAGACAGAGGCTCTGTGGAGATCTGGCGGTTGCTTGTGAG 600
OY 601 GTGGGCTTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
    |||||
Db 601 GTGGGCTTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
OY 661 CACATTTCTGCGGACACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
    |||||
Db 661 CACATTTCTGCGGACACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
OY 721 ACCTGACATCTATGACACATCTGACAGGAGGAGGAGGAGGAGGAGGAG 780
    |||||
Db 721 ACCTGACATCTATGACACATCTGACAGGAGGAGGAGGAGGAGGAGGAG 780
OY 781 TTGAGAGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 820
    |||||
Db 781 TTGAGAGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 820

```

RESULT 3
AC022505
LOCUS AC022505
DEFINITION Homo sapiens clone RP11-349C2, WORKING DRAFT SEQUENCE, 21 unordered
pieces.
AC022505
VERSION AC022505.17 GI:20335463
KEYWORDS HTG: HTGS_PHASE1, HTGS_DRAFT.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 191078)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Alsbrooks,S.L., Amarantunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbata,J., Benton,J., Bimaye,K., Blankenburg,K., Bonin,D.,
Bouck,J., Bowe,S., Brileva,M., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carton,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,K., Dathorne,S.R., David,R.,
Della,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dith,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escoto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisl,A., Geo,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlik,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hognes,M., Holloway,C., Hollins,B.,
Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,T.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louised,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapa,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mel,G., Metzger,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabath,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenwo,S., Ogun,M., Okunnu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Plickens,R., Primus,E., Pull,L., Qulles,M., Ren,Y.,
Rivers,M., Rojas,A., Rojokokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scheher,E., Soneike,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tameris,A., Tameris,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Tsunai,K., Vaequez,L., Vera,V., Villalón,D., Vinson,R., Wang,O.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wellington,S.,
Williams,G., Williamson,A., Wleciyk,R., Woden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gldbs.R.

Direct Submission
Unpublished
2 (bases 1 to 191078)
Submitted (05-FEB-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 191078)
Submitted (09-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Apr 28, 2002 this sequence version replaced gi:16117888.

Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: HADS
Center clone name: RP11-349C2
Sequencing vector: M13
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 17422 bases at least Q40
Consensus quality: 181742 bases at least Q30
Consensus quality: 186048 bases at least Q20
Estimated insert size: 185777; sum-of-contrigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contrigs estimation

* NOTE: Estimated insert size may differ from sequence length

```
* (see http://www.birc.bcm.tmc.edu/docs/genbankdraft.data.html)
*
* NOTE: This is a 'working draft' sequence. It currently
* consists of 21 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
```

1	2636: contig of 2636 bp in length
2	2737: gap of unknown length
3	2737: contig of 2179 bp in length
4	5015: gap of unknown length
5	5016: contig of 2959 bp in length
6	7975: gap of unknown length
7	8075: contig of 2013 bp in length
8	10088: gap of unknown length
9	10188: contig of 3121 bp in length
10	13309: gap of unknown length
11	13409: contig of 5664 bp in length
12	19072: gap of unknown length
13	19173: contig of 4137 bp in length
14	22310: gap of unknown length
15	22310: contig of 5098 bp in length
16	28308: gap of unknown length
17	28608: contig of 3358 bp in length
18	31965: gap of unknown length
19	32066: contig of 6548 bp in length
20	32066: contig of 6548 bp in length
21	38614: gap of unknown length
22	38714: contig of 5752 bp in length
23	44465: gap of unknown length
24	44466: contig of 4629 bp in length
25	44566: gap of unknown length
26	49194: contig of 4629 bp in length
27	49195: gap of unknown length
28	49295: contig of 9563 bp in length
29	58858: gap of unknown length
30	58958: contig of 7528 bp in length
31	66455: gap of unknown length
32	66486: contig of 10872 bp in length
33	66586: gap of unknown length
34	77457: contig of 13968 bp in length
35	77458: gap of unknown length
36	91545: contig of 13968 bp in length
37	91546: gap of unknown length
38	91645: gap of unknown length
39	107288: contig of 15643 bp in length
40	107388: gap of unknown length
41	107389: contig of 14176 bp in length
42	121564: gap of unknown length
43	121565: contig of 15305 bp in length
44	136969: gap of unknown length
45	137070: contig of 16528 bp in length
46	153597: gap of unknown length
47	153598: contig of 16528 bp in length
48	153598: gap of unknown length
49	153598: contig of 37381 bp in length

FEATURES	
source	Location/Qualifiers
1.	1.191078
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone-RP11-349C2"
BASE COUNT	37980 a 55810 c 56330 g 38874 t 2084 others
ORIGIN	

Query Match	15.8%;	Score 400;	DB 2;	Length 191078;
Best Local Similarity	99.5%;	Pred. No. 4.9e-190;		
Matches 740;	Conservative 0;	Mismatches 2;	Indels 2;	Gaps 2

QY	70	CTGAGGTTGGGGGGCCCTCAGTGGCTGTGTCCAGCCGGGTGGGCTCTGGAGACCTTT	129
Db	154269	CTTGAGGTTGGGGGGCCCTCAGTGGCTGTGTCCAGCCGGGTGGGCTCTGGAGACCTTT	1543289
QY	130	TCTGAGGAGGAGGACGCTGTGTCTTGTGCCCTCAGAGAGCTCTGGAGCTGGAGGAGACCTTGAC	189
Db	154329	TCTGAGGAGGAGGACGCTGTGTCTTGTGCCCTCAGAGAGCTCTGGAGCTGGAGGAGACCTTGAC	1543888
QY	190	CTGAGCGAGCCTTCTCCTTTCACCCGCCCGGGGCACT-CTCCGGTGTGGAGACCCCAAGGCTTT	248
Db	154389	CTGAGCGAGCCTTCTCCTTTCACCCGCCCGGGGCACTCTCCGGTGTGGAGACCCCAAGGCTTT	154448

QY	249	TCCTGGACATGGGGCAGAGAGTAGGTTTCTCTGGACACAGAAACCATTAAGACGTTATT	308
Db	15449	TCCTGGACATGGGGCAGAGAGTAGGTTTCTCTGGACACAGAAACCATTAAGACGTTATT	154508
QY	309	TAGCTGTGTTTGTGTGGGGGAGGTCAGAGCCCATCCAAAAGGCTCTCCCTACCCCTGGC	368
Db	154509	TAGCTGTGTTTGTGTGGGGGAGGTCAGAGCCCATCCAAAAGGCTCTCCCTACCCCTGGC	154568
QY	369	TGCTTGGAGGCAAGAGATGCAACCCGCCGCAACTCCACAGCTGCCCCCTCCACGTTAGAC	428
Db	154569	TGCTTGGAGGCAAGAGATGCAACCCGCCGCAACTCCACAGCTGCCCCCTCCACGTTAGAC	154627
QY	429	CGTTGGCTGCATACAGCGCTGAAGCCACTGTACACACAGAGAGCCCTTGGCATGCAAGAGA	488
Db	154628	CGTTGGCTGCATACAGCGCTGAAGCCACTGTACACACAGAGAGCCCTTGGCATGCAAGAGA	154687
QY	489	GGGGACGCTGTGGCCCTTGGCCCTCTGTGAGGGGGTTAGGGGGAGCAAGGCTCTTCCCT	548
Db	154688	GGGGACGCTGTGGCCCTTGGCCCTCTGTGAGGGGGTTAGGGGGAGCAAGGCTCTTCCCT	154747
QY	549	AGCAAGAACAGAGGCTCTCTGGGAATGTGGCGGTGCGCGTTTGCTTAAAGCGAGTCGGCTT	608
Db	154748	AGCAAGAACAGAGGCTCTCTGGGAATGTGGCGGTGCGCGTTTGCTTAAAGCGAGTCGGCTT	154807
QY	609	ACAGCAGTACTTCTTCCACACTCAGCACAGCACACAGACACTGAGTGGAGTGGACATTCC	668
Db	154808	ACAGCAGTACTTCTTCCACACTCAGCACAGCACACAGACACTGAGTGGAGTGGACATTCC	154867
QY	669	CTGGCCAAACCAAGGAGGCTGAGAGGGGCTGGGCAACATGGGGCGGACCCACCTGGAC	728
Db	154868	CTGGCCAAACCAAGGAGGCTGAGAGGGGCTGGGCAACATGGGGCGGACCCACCTGGAC	154927
QY	729	ATCTATGACCACTGCGACAGTCGAGGATGCTTGTCTGACAGGACAGAGCTCCCTTGAAGA	788
Db	154928	ATCTATGACCACTGCGACAGTCGAGGATGCTTGTCTGACAGGACAGAGCTCCCTTGAAGA	154987
QY	789	AGCTTGCTATTGTGTGATGAGGAG 812	
Db	154988	AGCTTGCTATTGTGTGATGAGGAG 155011	

RESULT 4				
LOCUS	HSU16258	1813 bp	mRNA	linear
DEFINITION	Human I kappa B mRNA, complete cds.			
ACCESSION	U16258			
VERSION	U16258.1	GI:746414		
KEYWORDS				
SOURCE	Homo sapiens.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 325 to 1770)			
AUTHORS	Ray, P., Zhang, D.H., Elias, J.A. and Ray, A.			
TITLE	Cloning of a differentially expressed I kappa B-related protein			
JOURNAL	J. Biol. Chem. 270 (18), 10680-10685 (1995)			
MEDLINE	95256234			
PUBMED	7738005			
REFERENCE	2 (bases 1 to 1813)			
AUTHORS	Ray, A.			
TITLE	Direct Submission			
JOURNAL	Submitted (24-OCT-1994) Anuradha Ray, Internal Medicine/Pulmonary			

FEATURES	Location/Qualifiers
source	1. .1813

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="HeLa S3"
1..324
5'UTR
CDS
325..1770
/function="inhibitor of transcription factor NF kappa B"

```

```

/codon_start=1
/product="I kappa BR"
/protein_id="AAA85819.1"
/db_xref="GI:746415"
/translation="MKTRLYLNLGTFESLQOTALCNDFKRSIFLADENHLYEDLFR
ANYNGITLHWRAGHSGOAMRCLEGAECARHMESEAVHGRVLRGCTGPPRGRLFGC
QASPEALDQAIPEACAEBSHLEPPACAAVRLQOOLEEAGRGPOGMVACEQIDG
LESKADPEAPRAEAYOKOLRPAFLDLRPGARAIIVHSATTLGMDKHGAVRHDE
ELRSGVNLGEAKTMINITALSREARCRAGAPVLPESAOICPAGSPSPAPAGLAA
SPYRAEGCRPEAPETRLRLRELSAEDDEFEPEAREBAPASGERTPGRRGALREA
GHRMPDPAAGSGRSGSPPGCAKSKMNRNDMGTLLHRACIRQURVODLVKQG
HPLNPRDYCGWTPLEHACVGHLEIVRELLDHAADVDPGGGCEGTPPLHDALNCGH
FEVALLERGGSVTLRTRKASARWRRCSSG"
repeat_region
1435..1734
/rpl_family="ankyrin"
3'UTR
1771..>1813
BASE COUNT      382 a      530 c      591 g      310 t
ORIGIN
      13.5%; Score 340; DB 9; Length 1813;
      100.0%; Pred. No. 1.6e-159;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Query Match
1923 AAGGGAGCAAGTGGCAACCGGGAACGACATGGGGAGACCTGCTGCACGAGCCTGC 1982
      |||
1396 AAGGGAGCAAGTGGCAACCGGGAACGACATGGGGAGACCTGCTGCACGAGCCTGC 1455
      |||
1983 ATCGAGGGCAGCTGGCGCGCGCTGCAGACCTGTGAGGAGGAGGCGACCCCTTAACCT 2042
      |||
1456 ATCGAGGGCAGCTGGCGCGCGCTGCAGACCTGTGAGGAGGAGGCGACCCCTTAACCT 1515
      |||
2043 CGGAGCTACTGTGGCTGGACACCTGTGCAGAGGCTGCAACTAGCGGCAATCTAGAATT 2102
      |||
1516 CGGAGCTACTGTGGCTGGACACCTGTGCAGAGGCTGCAACTAGCGGCAATCTAGAATT 1575
      |||
2103 GTCCGCTTCTGCTGGACACCGGGGCGGAGTGGAGACCCAGGTGGCCAGGGCTCGGAA 2162
      |||
1576 GTCCGCTTCTGCTGGACACCGGGGCGGAGTGGAGACCCAGGTGGCCAGGGCTCGGAA 1635
      |||
2163 GGCATACACCCCTCCACATGCTGCTCACTGTCGCTGAGGTGGCTGAGCTGCTG 2222
      |||
1636 GGCATACACCCCTCCACATGCTGCTCACTGTCGCTGAGGTGGCTGAGCTGCTG 1695
      |||
2223 CTTGAACGGGGGGCGCTCGCTACCTCCGCACTCGAAGAAG 2262
      |||
1696 CTTGAACGGGGGGCGCTCGCTACCTCCGCACTCGAAGAAG 1735
      |||

```

```

TITLE
JOURNAL
REFERENCE
AUTHORS
Lohoczky, J., Levine, R., Liu, G., Maclean, C., Macdonald, P.,
Marquis, N., Matthews, C., McCarthy, M., McKean, P., McKernan, K.,
McPheters, R., Meldrum, J., Menus, L., Mihova, T., Mienna, V.,
Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H.,
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,
Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,
Roy, A., Santos, R., Schauer, S., Schnupack, R., Seaman, S., Severy, P.,
Sounez, C., Spencer, B., Strange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
Travers, M., Travis, N., Trigglio, J., Vassiliev, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (28-DEC-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
(bases 1 to 69215)
Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N.,
Anderson, S., Bara, N., Bastien, V., Bloom, T., Boguslavsky, L.,
Boukhgalter, B., Brown, A., Camarata, J., Campoliano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Larocque, K., Lamazares, R.,
Lander, T., Lohoczky, J., Levine, R., Lindblad-Toh, K., Liu, G.,
Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McKean, P., McKernan, K., Meldrum, J., Menus, L.,
Mihova, T., Mienna, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schnupack, R.,
Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigglio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (12-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 12, 2002 this sequence version replaced g1:1193983.
All repeats were identified using RepeatMasker:
smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center -----
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information -----
Center project name: L11607
Center clone name: 349_C-2
NOTE: This record contains 85 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1
721 820: contig of 720 bp in length
821 1513: contig of 693 bp in length
1514 1613: gap of 100 bp
1614 2351: contig of 738 bp in length
2352 2451: gap of 100 bp
2452 3143: contig of 692 bp in length

```



```

* 3144 3243: gap of 100 bp
* 3244 4033: contig of 790 bp in length
* 4034 4133: gap of 100 bp
* 4134 4825: contig of 692 bp in length
* 4826 4925: gap of 100 bp
* 4926 5649: contig of 724 bp in length
* 5650 5749: gap of 100 bp
* 5750 6464: contig of 715 bp in length
* 6465 6564: gap of 100 bp
* 6565 7272: contig of 708 bp in length
* 7273 7372: gap of 100 bp
* 7373 8069: contig of 697 bp in length
* 8070 8169: gap of 100 bp
* 8170 8884: contig of 715 bp in length
* 8885 8984: gap of 100 bp
* 8985 9724: contig of 740 bp in length
* 9725 9824: gap of 100 bp
* 9825 10535: contig of 709 bp in length
* 10534 10633: gap of 100 bp
* 10634 11363: contig of 730 bp in length
* 11364 11463: gap of 100 bp
* 11464 12178: contig of 715 bp in length
* 12179 12278: gap of 100 bp
* 12279 12996: contig of 718 bp in length
* 12997 13096: gap of 100 bp
* 13097 13810: contig of 714 bp in length
* 13811 13910: gap of 100 bp
* 13911 14621: contig of 711 bp in length
* 14622 14721: gap of 100 bp
* 14722 15433: contig of 712 bp in length
* 15434 15533: gap of 100 bp
* 15534 16257: contig of 724 bp in length
* 16258 16357: gap of 100 bp
* 16358 17070: contig of 713 bp in length
* 17071 17170: gap of 100 bp
* 17171 17839: contig of 669 bp in length
* 17840 17939: gap of 100 bp
* 17940 18628: contig of 689 bp in length
* 18629 18728: gap of 100 bp
* 18729 19444: contig of 716 bp in length
* 19445 19544: gap of 100 bp
* 19545 20254: contig of 710 bp in length
* 20255 20354: gap of 100 bp
* 20355 21063: contig of 729 bp in length
* 21064 21183: gap of 100 bp
* 21184 21910: contig of 727 bp in length
* 21911 22010: gap of 100 bp
* 22011 22738: contig of 728 bp in length
* 22739 22838: gap of 100 bp
* 22839 23553: contig of 715 bp in length
* 23554 23653: gap of 100 bp
* 23654 24374: contig of 721 bp in length
* 24375 24474: gap of 100 bp
* 24475 25193: contig of 719 bp in length
* 25194 25293: gap of 100 bp
* 25294 26037: contig of 744 bp in length
* 26038 26137: gap of 100 bp
* 26138 26860: contig of 723 bp in length
* 26861 26960: gap of 100 bp
* 26961 27665: contig of 705 bp in length
* 27666 27765: gap of 100 bp
* 27766 28471: contig of 706 bp in length
* 28472 28571: gap of 100 bp
* 28572 29282: contig of 711 bp in length
* 29283 29382: gap of 100 bp
* 29383 30106: contig of 724 bp in length
* 30107 30206: gap of 100 bp
* 30207 30896: contig of 690 bp in length
* 30897 30996: gap of 100 bp
* 30997 31719: contig of 723 bp in length
* 31720 31819: gap of 100 bp
* 31820 32532: contig of 713 bp in length
* 32533 32632: gap of 100 bp

```

```

* 32633 33342: contig of 710 bp in length
* 33343 33442: gap of 100 bp
* 33443 34165: contig of 723 bp in length
* 34166 34265: gap of 100 bp
* 34266 34973: contig of 708 bp in length
* 34974 35073: gap of 100 bp
* 35074 35773: contig of 700 bp in length
* 35774 35873: gap of 100 bp
* 35874 36586: contig of 713 bp in length
* 36587 36686: gap of 100 bp
* 36687 37406: contig of 720 bp in length
* 37407 37506: gap of 100 bp
* 37507 38215: contig of 709 bp in length
* 38216 38315: gap of 100 bp
* 38316 39042: contig of 727 bp in length
* 39043 39142: gap of 100 bp
* 39143 39874: contig of 732 bp in length
* 39875 39974: gap of 100 bp
* 39975 40698: contig of 724 bp in length
* 40699 40798: gap of 100 bp
* 40799 41486: contig of 688 bp in length
* 41487 41586: gap of 100 bp
* 41587 42300: contig of 714 bp in length
* 42301 42400: gap of 100 bp
* 42401 43019: contig of 619 bp in length
* 43020 43119: gap of 100 bp
* 43120 43834: contig of 715 bp in length
* 43835 43934: gap of 100 bp
* 43935 44656: contig of 722 bp in length
* 44657 44756: gap of 100 bp
* 44757 45441: contig of 685 bp in length

```

```

Query Match          5.5%: Score 138; DB 2: Length 69215;
Best Local Similarity 100.0%: Pred. No. 5.2e-58;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 70 CTTGCAGGTGCGGGCGCCCTCACTGCGCTGTCACAGCCCGGTGCGCCTTGAGCCCTTT 129
      |||||||
DB 49068 CTTGCAGGTGCGGGCGCCCTCACTGCGCTGTCACAGCCCGGTGCGCCTTGAGCCCTTT 49069
QY 130 TCTGAGAGGAGGAGGCGCTGCTTTCCGCGTCAGAGGCTTGAGGCGACACCTGAC 189
      |||||||
DB 49008 TCTGAGAGGAGGAGGCGCTGCTTTCCGCGTCAGAGGCTTGAGGCGACACCTGAC 48949
QY 190 CTGACGACGCTTGCCCTT 207
      |||||||
DB 48948 CTGACGACGCTTGCCCTT 48931

```

Search completed: May 27, 2003, 11:08:57
Job time : 7346 secs

Search completed: May 27, 2003, 09:06:15
Job time : 568 secs

RESULT 2

ABL80248/C
ID ABL80248 standard; cDNA; 302 BP.

XX ABL80248;

DT 17-MAY-2002 (first entry)

XX Human ovarian cancer related cDNA clone SEQ ID NO:3226.

DE Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.

XX Homo sapiens.

OS WO200192581-A2.

XX 06-DEC-2001.

PD 29-MAY-2001; 2001WO-US17756.

XX 26-MAY-2000; 2000US-207484P.

PA (CORI-) CORIXA CORP.

XX Algate PA, Harlocker SL, Jones R;

DR WPI; 2002-122075/16.

XX Composition for therapy and diagnosis of ovarian cancer comprising

PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding

PT polypeptide, antibody specific to polypeptide or T cell expressing

PT polypeptide -

XX Claim 1; SEQ ID 3226; 489pp; English.

XX The present invention describes a composition (I) comprising: carriers

CC and immunostimulants; and a polypeptide (II) of a ovarian tumour

CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence

CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to

CC ABL7934, (III) encoding (II) having a sequence (S2), a T cell

CC population of (II), or antigen presenting cells that express (II).

CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to

CC (S1) can be used for detecting ovarian cancer in a patient's biological

CC sample preferably serum or ovarian tissue. The method comprises

CC contacting a biological sample from a patient with (IV), detecting the

CC amount of polynucleotide hybridising to (IV) and comparing the amount to

CC a predetermined cutoff value and thereby detecting ovarian cancer in the

CC patient, where the amount of polynucleotide hybridising to (IV) is

CC detected preferably by polymerase chain reaction (PCR). (I) comprising

CC (II) and/or (II) is useful for stimulating and/or expanding T cells

CC specific for an ovarian tumour protein comprising contacting T cells

CC with (III) or (II). (III) is useful in design and preparation of

CC ribozyme molecules for inhibiting expression of the tumour polypeptides

CC and proteins in tumour cells; and to isolate a full length gene from a

CC suitable library e.g., a tumour cDNA library using well known

CC techniques.

CC Sequence 302 BP; 59 A; 96 C; 108 G; 39 T; 0 other;

CC Query Match 4.0%; Score 101; DB 24; Length 302;

CC Best Local Similarity 100.0%; Pred. No. 9.9e-36;

CC Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 0Y 2096 AGAATTTGCGCTTCGCTGACGAGGCGCGACAGTGCAGCCAGGTGGCCAGG 2155

CC DB 260 AGAATTTGCGCTTCGCTGACGAGGCGCGACAGTGCAGCCAGGTGGCCAGG 201

CC 0Y 2156 CTGCGAAGGCAATCAGCCCGCTCCAGATGCCCTCAACTGTG 2196

CC DB 200 CTGCGAAGGCAATCAGCCCGCTCCAGATGCCCTCAACTGTG 160

GenCore version 5.1.4-p5-4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 08:59:22 ; Search time 95 Seconds
(without alignments)
8151.146 Million cell updates/sec

Title: US-09-993-731-10

Perfect score: 2525
Sequence: 1 ctctgggctgtgcccgtggcc.....cgcattctctctccacacaga 2525

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 100

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query			
No.	Score	Match	Length	ID
Description				
No matches found				

Search completed: May 27, 2003, 11:58:01
Job time : 98 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 11:09:37; Search time 338 Seconds
(without alignments)

9864.400 Million cell updates/sec

Title: US-09-993-731-10

Perfect score: 2525
Sequence: 1 ctcctggcgtgctgcctgccc.....cgcattctctctccacaga 2525

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 828747 seqs, 660231138 residues

Word size: 100

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database: Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCr_NEM_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEM_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEM_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCrUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEM_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_NEM_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEM_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEM_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	167	6.6	443	10	US-09-867-701-10730
C 2	101	4.0	302	10	US-09-867-701-3226

ALIGNMENTS

RESULT 1
US-09-867-701-10730/c
; Sequence 10730, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701

CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 10730
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(443)
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-10730

Query Match 6.6%; Score 167; DB 10; Length 443;
Best Local Similarity 100.0%; Pred. No. 8e-73;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2096 AGAATTTGTCGCTTCTGCTGAGACACGAGGCGGAGTGAGACGACCCAGTGCCAGGG 2155
DB 262 AGAATTTGTCGCTTCTGCTGAGACACGAGGCGGAGTGAGACGACCCAGTGCCAGGG 203
QY 2156 CTGCGAAGGATCACCCCTCCACGATGCGCTCACTGAGGCGCAGTGGGCTGA 2215
DB 202 CTGCGAAGGATCACCCCTCCACGATGCGCTCACTGAGGCGCAGTGGGCTGA 143
QY 2216 GCTGCTGCTTGAACGGGGGCGTCCGTCACCTCCGCACTCGAAGG 2262
DB 142 GCTGCTGCTTGAACGGGGGCGTCCGTCACCTCCGCACTCGAAGG 96

RESULT 2
US-09-867-701-3226/c
; Sequence 3226, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3226
; LENGTH: 302
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-3226

Query Match 4.0%; Score 101; DB 10; Length 302;
Best Local Similarity 100.0%; Pred. No. 5.2e-40;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2096 AGAATTTGTCGCTTCTGCTGAGACACGAGGCGGAGTGAGACGACCCAGTGCCAGGG 2155
DB 260 AGAATTTGTCGCTTCTGCTGAGACACGAGGCGGAGTGAGACGACCCAGTGCCAGGG 201
QY 2156 CTGCGAAGGATCACCCCTCCACGATGCGCTCACTGAGGCGCAGTGGGCTGA 2216
DB 200 CTGCGAAGGATCACCCCTCCACGATGCGCTCACTGAGGCGCAGTGGGCTGA 160

Search completed: May 27, 2003, 13:57:18
Job time: 341 secs

GenCore version 5.1.4_P5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 08:51:45 ; Search time 3520 Seconds
(without alignments)
11617.501 Million cell updates/sec

Title: US-09-993-731-10

Perfect score: 2525

Sequence: 1 ctctcgagctgtgcctgtgccc.....cgactctctctccacaga 2525

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 100

Total number of hits satisfying chosen parameters: 21

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST:*
1: em_estba:*
2: em_esthu:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pin:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	703	27.8	817	14	BQ230076 AGENCOURT
2	680	26.9	1096	13	BM463971 AGENCOURT
3	491	19.4	970	14	BM903924 AGENCOURT
4	486	19.2	1170	13	BM477754 AGENCOURT
5	449	17.8	929	14	BM960372 AGENCOURT
6	388	15.4	682	10	BM407508 AGENCOURT

ALIGNMENTS

7	236	9.3	1784	14	B0057501 AGENCOURT
8	194	7.7	492	13	BM193972 AGENCOURT
9	180	7.1	421	10	BE383502 AGENCOURT
10	180	7.1	1101	12	BE314727 AGENCOURT
11	167	6.6	443	9	A1733922 AGENCOURT
12	167	6.6	503	9	A1820902 AGENCOURT
13	167	6.6	543	12	BF111950 AGENCOURT
14	148	5.9	699	12	BG392570 AGENCOURT
15	136	5.4	506	9	A1821538 AGENCOURT
16	136	5.4	506	9	A1821587 AGENCOURT
17	132	5.2	476	12	BG474073 AGENCOURT
18	131	5.2	347	14	BQ379444 AGENCOURT
19	121	4.8	483	12	BF954610 AGENCOURT
20	117	4.6	477	9	A1570434 AGENCOURT
21	101	4.0	302	9	AA293771 AGENCOURT

RESULT 1
BQ230076
LOCUS BQ230076
DEFINITION BQ230076 817 bp mRNA linear EST 02-MAY-2002
ACCESSION AGENCOURT_7558812 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6045468
VERSION BQ230076
KEYWORDS 5', mRNA sequence.
SOURCE BQ230076.1 GI:20411476
ORGANISM human.
REFERENCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 817)
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapds@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LRAM13289 row: 1 column: 13
High quality sequence stop: 687.
Location/Qualifiers
1..817
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6045468"
/clone_id="NIH_MGC_92"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: PCMV-SPORE6; Site:1: NotI; Site:2: SalI; Cloned unidirectionally; Oligo dt primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
BASE COUNT 165 a 254 c 287 g 110 t 1 others
ORIGIN

Query Match 27.8%, Score 703; DB 14; Length 817;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 753; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1519 GCGGACAGCTGCTGGAGAGGCGCAAGACCTGCTGACATGCACTGCCGCGAGAGG 1578
|||||
DB 1 GCGGACAGCTGCTGGAGAGGCGCAAGACCTGCTGACATGCACTGCCGCGAGAGG 60
|||||
QY 1579 CCGGAGATCCAGCAGCTGCTGGCGCGCTGCTTCAGAAAGCCCTGAGCTGTCTCAGC 1638
|||||

QY	1639	AGGCCCCAGCGCTGCCCGACCTGCAGAGGCGAGTCTTGGACAGCATCTTCCATACCGGTGCAGCTGA	1698
Db	121	AGGCCCCAGCGCTGCCCGACCTGCAGAGGCGAGTCTTGGACAGCATCTTCCATACCGGTGCAGCTGA	180
QY	1699	GGCTGCAGAGCCCCAGAGAGGCCCTTGAGACCCGAACCAACACTGCGGGAGCTCAGTGTACTGTG	1758
Db	181	GGCTGCAGAGCCCCAGAGAGGCCCTTGAGACCCGAACCAACACTGCGGGAGCTCAGTGTACTGTG	240
QY	1759	AGATGTAAGATGTAGAGAGGAGGAGCGGAGGAGGCGGACGCCACACACCGGAGAGGGAAGGCC	1818
Db	241	AAAGTAAAGATGTAGAGAGGAGGAGCGGAGGAGGCGGACGCCACACACCGGAGAGGGAAGGCC	300
QY	1819	TGAGAGCGCGGCGAGGAGTGAGACTCTCCAGAGAGGCGGAGAGCAGCACCACTATGGCTTACCCCGC	1878
Db	301	TGAGAGCGCGGCGAGGAGTGAGACTCTCCAGAGAGGCGGAGAGCAGCACCACTATGGCTTACCCCGC	360
QY	1879	AGCTGAGAGAGAGCAGAGGAGCTTCAGAGGCCACCTGGGCGCGGCGGAGGAGGAGCAGAGTGA	1938
Db	361	AGCTGAGAGAGAGCAGAGGAGCTTCAGAGGCCACCTGGGCGCGGCGGAGGAGGAGCAGAGTGA	420
QY	1939	ACCGGCGAAACGAGCATGGGGGAGAACCTCTGTGTACCCGAGCTTGCAATCGAGAGGCCAGCTGC	1998
Db	421	ACCGGCGAAACGAGCATGGGGGAGAACCTCTGTGTACCCGAGCTTGCAATCGAGAGGCCAGCTGC	480
QY	1999	GCCGCGTCACGAGACCTTGTAGAGCAAGGCGCACCCCTTAAACCTCGGGAGTACTGTGGCT	2058
Db	481	GCCGCGTCACGAGACCTTGTAGAGCAAGGCGCACCCCTTAAACCTCGGGAGTACTGTGGCT	540
QY	2059	GGACACCTCTGCACAGAGGCGCTGCACTACGGGCATTTAGAAATTTGCCCTTCTGCTGG	2118
Db	541	GGACACCTCTGCACAGAGGCGCTGCACTACGGGCATTTAGAAATTTGCCCTTCTGCTGG	600
QY	2119	ACCACGGGGGCGCCAGTGGAGCAGACCCAGTGGGCGAGGCGTGCAGAAAGGCATCACCCCGCTGC	2178
Db	601	ACCACGGGGGCGCCAGTGGAGCAGACCCAGTGGGCGAGGCGTGCAGAAAGGCATCACCCCGCTGC	660
QY	2179	ACGATGGCCCTCAACTGTGGCCACTTGGAGGTGGCTGAGTGTCTTGAAGCGGGGGCGT	2238
Db	661	ACGATGGCCCTCAACTGTGGCCACTTGGAGGTGGCTGAGTGTCTTGAAGCGGGGGCGT	720
QY	2239	CCGTCAACCTCCGCACTCGAAAGGGGCGTCAAGCC	2272
Db	721	CCGTCAACCTCCGCACTCGAAAGGGGCGTCAAGCC	754
SOUT 2	63971		
LOCUS	63971		
DEFINITION	BM463971	1096 bp	mRNA linear EST 05-PEB-2002
ACCESSION	AGNCNCOURT.6445689	NIH_MGC_72	Homo sapiens cDNA clone IMAGE:553988
VERSION	BM463971		
KEYWORDS	BM463971.1	GI:18513013	
SOURCE	EST.		
ORGANISM	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 1096)		
JOURNAL	NIH-MGC hftp://mgc.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapsb-remail.nih.gov		
	Tissue Procurement: ATCC/DC/DTP		
	cDNA Library Preparation: Life Technologies, Inc.		
	DNA sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LMD at:		
	hftp://image.lnl.gov		
	Plate: L1AM1235	row: f	column: 21

FEATURES									
High quality sequence stop: 682.									
Location/Qualifiers									
1. .1096									
/organism="Homo sapiens"									
/db_xref="taxon:9606"									
/clone="IMAGE:553988"									
/clone_lib="NIH.MGC.72"									
/tissue_type="melanotic melanoma"									
/lab_host="DH10B (phage-resistant)"									
/note="Organ: SKIN; Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."									
BASE COUNT									
217 a 371 c 362 g 146 t									
ORIGIN									
Query Match 26.9%; Score 680; DB 13; Length 1096;									
Best Local Similarity 99.9%; Pred. No. 0;									
Matches 730; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	1432	TCCACGTGTCCTCGGCGCACACACACTGGGAGACATGAAGACCACTAGTGGCGGTGGCC	1491						
DB	26	TCCACGTGTCCTCGGCGCACACACTGGGAGACATGAAGACCACTAGTGGCGGTGGCC	85						
QY	1492	ACTATGAGGAGAACTGAGGCTGCCAGCGGCACAGCTGCTGGAGAGCCAAAGACTGGC	1551						
DB	86	ACTATGAGGAGAACTGAGGCTGCCAGCGGCACAGCTGCTGGAGAGCCAAAGACTGGC	145						
QY	1552	TGACCAATTGACATCTGCCCCGAGAGAGGCCGGGAGATGCTACGACCTGTGGCCCCGTGCT	1611						
DB	146	TGAACATTGCACTGTCCCGGAGAGAGCCGGGAGATGCCCTACGACCTCTGCCCCGTGCT	205						
QY	1612	TCCAGAAAGCGCTACAGCTGTGCTCAGCAGAGGCCACAGCTGCCACCTCAGAGGCGAGTCT	1671						
DB	206	TCCAGAAAGCGCTACAGCTGTGCTCAGCAGAGGCCACAGCTGCCACCTCAGAGGCGAGTCT	265						
QY	1672	TGCGACATCTCCATACCCGTGCAGCTGAGGCTGTCAGCCCCAGAGAGCCCTTGAGACCGAA	1731						
DB	266	TGCGACATCTCCATACCCGTGCAGCTGAGGCTGTCAGCCCCAGAGAGCCCTTGAGACCGAA	325						
QY	1732	CCAGACTGCGGGAGCTCAGTGTAGCTGAAGATGAAGATGAGAGAGAGGAGGAGAGG	1791						
DB	326	CCAGACTGCGGGAGCTCAGTGTAGCTGAAGATGAAGATGAGAGAGAGGAGGAGAGG	385						
QY	1792	CGGACGCCACAGCGGAGAGCGAAGCCCTGAGGCCCGCGGAGGTGGAGCTCTCAGAGAGCG	1851						
DB	386	CGGACGCCACAGCGGAGAGCGAAGCCCTGAGGCCCGCGGAGGTGGAGCTCTCAGAGAGCG	445						
QY	1852	AGGAGGACACCGATGGCTGACCCCGCAGCTGAGAGAGAGAGAGAGACTTCAGAGGCCACC	1911						
DB	446	AGGAGGACACCGATGGCTGACCCCGCAGCTGAGAGAGAGAGAGAGACTTCAGAGGCCACC	505						
QY	1912	TGGGCGGGGAGGAGGAGCAAGTGGAAACCGGCAAAAGCATGGGGAGACCCCTCTGC	1971						
DB	506	TGGGCGGGGAGGAGGAGCAAGTGGAAACCGGCAAAAGCATGGGGAGACCCCTCTGC	565						
QY	1972	ACCGAGCCTGTCATCGAGGGCCAGCTGCGCGCGCTCCAGAGACTTGTGAGGCGAGGCCACC	2031						
DB	566	ACCGAGCCTGTCATCGAGGGCCAGCTGCGCGCGCTCCAGAGACTTGTGAGGCGAGGCCACC	625						
QY	2032	CCCTTAACCCCTGGGGCTCTGTGGCTGGAGACCTCGACAGAGGCGCTGCANAATTACGGGC	2091						
DB	626	CCCTTAACCCCTGGGGCTCTGTGGCTGGAGACCTCGACAGAGGCGCTGCANAATTACGGGC	685						
QY	2092	ATCTAGAAATTTGCGCTTCTGTGTGAGCAACGAGGGCGCAGTGGAGACCCAGGTGGCC	2151						
DB	686	ATCTAGAAATTTGCGCTTCTGTGTGAGCAACGAGGGCGCAGTGGAGACCCAGGTGGCC	745						
QY	2152	AGGGCTGCGGAA 2162							
DB	746	AGGGCTGCGGAA 756							

RESULT 3	BM903924	970 bp	mRNA	linear	EST 12-MAR-2002
LOCUS	BM903924				IMAGE:5492426
DEFINITION	AECNOOUTR 6695791 NH_MGC_67 Homo sapiens cDNA Clone IMAGE:5492426				
ACCESSION	BM903924				
VERSION	BM903924				
KEYWORDS	EST.				
SOURCE	human.				
SYNCHRON					

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 970)	NIH-MGC	http://mgc.ncl.nih.gov/	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1998)
	Contact: Robert Strausberg, Ph.D.			

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LNAW12114 row: 1 column: 03
High quality sequence: stop: 668.

FEATURES	SOURCE
Location/Qualifiers	1. '970
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="IMAGE:5492426"	
/clone_11b="NH_MGC_67"	
/tissue_type="retinoblastoma"	
/lab_host="DH10B (phage-resistant)"	
/note="Organ: eye; Vector: pCMV-SPORT6; Site: 1: Not; Site: 2: Salt; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Library constructed by Life Technologies."	
BASE COUNT	203 a 335 c 312 g 119 t 1 others
ORIGIN	

Query Match	19.48;	Score 491;	DB 14;	Length 970;
Best Local Similarity	99.88;	Pred. No. 3.2e-227;		
Matches 541; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

OY 1844 AGAGAGCGGACGACACCCTGGCCGTGACCCCGCAGCTGGAGGAGGACGAGGAGCTTCA 1903
|||||
|||||
Ob 1 AGAGAGCGGACGACACCCTGGCCGTGACCCCGCAGCTGGAGGAGGACGAGGAGCTTCA 60

2y 1904 GGGCCACCTGGGGCCGGCGGAAGGGGAGACAGTGGACCGGCGCAACGACATGGGGGAGAC 196
 |||||
 Db 61 GGGCCACCTGGGGCCGGCGGAAGGGGAGACAGTGGACCGGCGCAACGACATGGGGGAGAC 120

QY 1964 CCTGCTGCACCGAGCCTGCATTCGAGGGCCAGCTGCCGCCGCTCCAGGACTTGTGAGGCA 202
|||||
Db 121 CCTGCTGCACCGAGCCTGCATTCGAGGGCCAGCTGCCGCCGCTCCAGGACTTGTGAGGCA 180

Qy 2024 GGGCCACCCCCTTAACCCCTGGGACTACTGTGAGTGCACACCCTCGCACGAGGCCCTGCAA 208
Db 181 GGGCACCCTTAACCCCTGGGACTACTGTGAGTGCACACCCTCGCACGAGGCCCTGCAA 240			

Qy	2084	CTACGGGCATCTAGAAATTGTCGCCCTTCTGTGGACCACGGGCGCAGTGACGACC	214
Db	241	CTACGGGCATCTAGAAATTGTCGCCCTTCTGTGGACCACGGGCGCAGTGACGACC	300

Qy 2144 AGGTGGCCAGGSGCTGGCAAGCATCAACCCCCCTCCACGATGCCCTCAACTGTGGCCACTT 220
 |||||
 Db 301 AGTGGCCAGGSGCTGGCAAGCATCAACCCCCCTCCACGATGCCCTCAACTGTGGCCACTT 360

Qy 2204 CGAGGTGGCTGAGCTCTCTGCTTGACGGGGGGGTCCGTACCCCTCCGCACTCGAAGGG 226
|||
Db 361 CGAGGTGGCTGAGCTCTCTGCTTGACGGGGGGGGGTCCGTACCCCTCCGCACTCGAAGGG 420

Qy	2284	CCGAGCGCCCTGGAGACCTCAGCAGTGGGTGAACCTGTACCGCAGGACCTGGACCT	2323
Db	421	CCTAGCGCCCTGGAGACGTTGCAGCAGTGGGTGAAGCTGTACCGCAGGAGCCTGTGACCT	480
Qy	2334	GGAGACCGGGCAGAAAGCCAGGGCCCTGGAGATGCTGTCTCCAGGCGGGCTCCCTGGGGCA	2383
Db	481	GGAGACCGGGCAGAAAGCCAGGGCCCTGGAGATGCTGTCTCCAGGCGGGCTCCCTGGGGCA	540
Qy	2384	AG 2385	
Db	541	AG 542	

RESULT 4	BM477754	1170 bp	mRNA	linear	EST 05-FEB-2002
LOCUS	BM477754				
DEFINITION	BM477754	AGENCOUT_0485291 NIH-MGC_71	Homo sapiens	CDNA clone IMAGE:5555018	
ACCESSION	BM477754	5', mRNA sequence.			
VERSION	BM477754.1	GI:18526796			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				

REFERENCE	1 (bases 1 to 1170)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC).
JOURNAL	Unpublished (1992)
COMMENT	Contact: Robert Strausberg, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
plate: LLAM12274 row: 1 column: 03
high quality sequence stop: 548.

```
source
1. 1170
/organism="Homo sapiens"
/db_xref="taxon:9606"
```

BASE COUNT	ORIGIN
240 a	420 c 332 g 177 t 1 others

Query Match	19.28;	Score 486;	DB 13;	Length 1170;
Best Local Similarity	99.88;	Pred. No. 9e-225;		
Matches 536; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY 1849 GCGAGGACGACACCGATGGCTGACCCCGCAGCTGGAGGAGGAGGAGCTTACGGGCC 1908
|||||
Db 46 GCGAGGACGACACCGATGGCTGACCCCGCAGCTGGAGGAGGAGGAGCTTACGGGCC 105

QY 1909 ACCCTGGGCGCGCGGAAGGGAGCAAGTGCACACCGCGGGAACGACATGGGGAGACCCCTTC 1968
|||||
Db 106 ACCTGGGCGCGCGGAAGGGAGCAAGTGCACACCGCGGGAACGACATGGGGAGACCCCTTC 165

QY 1669 TGCACCGAGCCTGCATCGAGGGGCCAGCTCCGCGCTCCAGACCTTGTGACGACGAGGCC 2038
|||||
Db 166 TGCACCGAGCCTGCATCGAGGGGCCAGCTCCGCGCTCCAGACCTTGTGACGACGAGGCC /225

QY 2029 ACCCCTTAACCCCTCGGACTACTGTGCTGACACCTCTGCACGAGGCTGCAAT...G 2088
|||||

Db 226 ACCCCCTTAACCTCTGGGACTACTGTGGCTGACACCTCTGACGAGGCTGCACTAGC 285

QY 2089 GGCATCTAGAAATTTGTCCTCTCTCTCTGTCGACACAGGGGGCCGACAGTACAGCAGGTG 2148

Db 286 GGCATCTAGAAATTTGTCCTCTCTCTCTGTCGACACAGGGGGCCGACAGTACAGCAGGTG 345

QY 2149 GCCAGGGCTGCGAAGGACATCACCCCTCCACAGATGCTCCACATGCTGCTGCTGAGG 2208

Db 346 GCCAGGGCTGCGAAGGACATCACCCCTCCACAGATGCTCCACATGCTGCTGCTGAGG 405

QY 2209 TGGCTAGCTGCTGCTTGAACGGGGGGCGTCCCTGACCCCTCCGACATCGAAAGGCTTCA 2268

Db 406 TGGCTAGCTGCTGCTTGAACGGGGGGCGTCCCTGACCCCTCCGACATCGAAAGGCTTCA 465

QY 2269 GCCCGCTGGAGAGCTGTCGACAGTGGTGAAGCTGTACCGAGGAGCTGACCTGAGAGA 2228

Db 466 GCCCGCTGGAGAGCTGTCGACAGTGGTGAAGCTGTACCGAGGAGCTGACCTGAGAGA 525

QY 2329 CGCGGACAGAGGCGCAGGCGCATGAGATGCTGCTCCAGGCGGCTGCTCGGCGCAAG 2385

526 CGCGGACAGAGGCGCAGGCGCATGAGATGCTGCTCCAGGCGGCTGCTCGGCGCAAG 582

RESULT 5
BQ960372 929 bp mRNA linear EST 21-ANG-2002
LOCUS AGEMCOURT_8923052 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6472657
DEFINITION 5', mRNA sequence.
ACCESSION BQ960372
VERSION BQ960372.1 GI:22375850
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 929)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM14006 row: p column: 02
High quality sequence stop: 662.
Location/Qualifiers
1..929
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6472657"
/clone_lib="NIH_MGC_71"
/tissue_type="telomysarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site: 1; NciI;
Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb.
BASIC COUNT 191 a 281 c 306 g 149 t 2 others
ORIGIN

Query Match 17.8%; Score 449; DB 14; Length 929;
Best Local Similarity 99.8%; Pred. No. 8.4e-207;
Matches 499; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 633 CAGCACCAGCAGCAGTCTGAGCTGGACATTCCTCGCAACACAGGAGCTGAG 692
|||||
Db 243 CAGCACCAGCAGCAGTCTGAGCTGGACATTCCTCGCAACACAGGAGCTGAG 302
|||||

QY 693 AGGGCTGGGCGACATCGCGCGCACCCACCTGAGACATCTATGACACTGCGAGTCCAGG 752

Db 303 AGGGCTGGGCGACATCGCGCGCACCCACCTGAGACATCTATGACACAGTCCAGTCCAGG 362

QY 753 GATGCTTGTGTCAGGACAGCTGCTTGAAGAGAGCTTGGCTATTGTGATGAGAG 812

Db 363 GATGCTTGTGTCAGGACAGCTGCTTGAAGAGAGCTTGGCTATTGTGATGAGAG 422

QY 813 TTGAGAGGAGACACTGGCCCGCAGGAGAGCTGATGATGAGACCCGCTATCTCAAC 872

Db 423 CTGAGAGGGAGACACTGGCCCGCAGGAGAGCTGATGATGAGACCCGCTATCTCAAC 482

QY 873 CTGGGCTCAGCTTGTGAGAGCTGTCAGACAGACAGCCCTGTCAGAGATTACTTCAGAG 932

Db 483 CTGGGCTCAGCTTGTGAGAGCTGTCAGACAGACAGCCCTGTCAGAGATTACTTCAGAG 542

QY 933 AGCATCTCTCTGGGAGCAGAACCCCTTACAGAGACCTATTCGCGCCGCTACAG 992

Db 543 AGCATCTCTCTGGGAGCAGAACCCCTTACAGAGACCTATTCGCGCCGCTACAG 602

QY 993 CTGGGACCATCTCAGTGGCGCGCGGCGCAGCACTCCAGGCTATGCGCTTGAAGGT 1052

Db 603 CTGGGACCATCTCAGTGGCGCGCGGCGCAGCACTCCAGGCTATGCGCTTGAAGGT 662

QY 1053 GCCCGGAGTGTGGGACACCATGAGGAGCGGTTCATGAGAGAGAGTGGCTGGTT 1112

Db 663 GCCCGGAGTGTGGGACACCATGAGGAGCGGTTCATGAGAGAGAGTGGCTGGTT 722

QY 1113 ATTGCACAGTCTCTCCAGA 1132

Db 723 ATTGCACAGTCTCTCCAGA 742

RESULT 6
BE407508 682 bp mRNA linear EST 21-JUL-2000
LOCUS 601300344F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3630371 5',
DEFINITION mRNA sequence.
ACCESSION BE407508
VERSION BE407508.1 GI:9343958
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 682)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov
Plate: LLM0518 row: g column: 12
High quality sequence stop: 661.
Location/Qualifiers
1..682
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3630371"
/clone_lib="NIH_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pORF7; Site: 1; XhoI;
Site: 2; EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACAGG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit

/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: ovary; Vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCGAGTGGAGGCGCGGCTTTTCTTTTCTTTT 3'] double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 107 a 168 c 152 g 76 t

ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 8.8e-70; Length 503;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2096 AGAATTTGCGCTTCTGCTGACACAGGGGCGCAGTGGACGACCCAGTGGCCAGG 2155
|||||
262 AGAATTTGCGCTTCTGCTGACACAGGGGCGCAGTGGACGACCCAGTGGCCAGG 203
|||||

OY 2156 CTGGCAAGCATACACCCCTCCAGATGCGCTCACTGCGCCTTGCAGGTGGCTGA 2215
|||||

DB 202 CTGGCAAGCATACACCCCTCCAGATGCGCTCACTGCGCCTTGCAGGTGGCTGA 143
|||||

OY 2216 GCTGCTGTTGAACGGGGGCGCTCCGTCACCTCCGACCTGGAAGG 2262
|||||

DB 142 GCTGCTGTTGAACGGGGGCGCTCCGTCACCTCCGACCTGGAAGG 96
|||||

RESULT 13
BF11950 543 bp mRNA linear EST 20-OCT-2000
LOCUS BF11950
DEFINITION IMAGE:3523585 3' similar to TR:09UGJ2 09UGJ2 IKAPPAHR ;, mRNA sequence.
IMAGE:3523585 3' similar to TR:09UGJ2 09UGJ2 IKAPPAHR ;, mRNA sequence.
BF11950
EST.
BF11950.1 GI:10941729

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 543)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: c9abps-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the IMAGE Consortium (infoimage.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 455.
Location/Qualifiers
1. 543
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3523585"
/clone_lib="Soares NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pec (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and clones: Soares NBHP pool 1: 309384-310919, 323208-325895 Soares NBHP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 -

150407, 151176-152327 Soares NB2HF8-9W pool 1: 758280-760583, 772104-774407 Soares NBHP pool 1: 304776-306311, 320136-322823, 326280-326663 Soares NBHP pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 91 a 161 c 172 g 119 t

ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 8.9e-70; Length 543;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2096 AGAATTTGCGCTTCTGCTGACACAGGGGCGCAGTGGACGACCCAGTGGCCAGG 2155
|||||

DB 320 AGAATTTGCGCTTCTGCTGACACAGGGGCGCAGTGGACGACCCAGTGGCCAGG 379
|||||

OY 2156 CTGGCAAGCATACACCCCTCCAGATGCGCTCACTGCGCCTTGCAGGTGGCTGA 2215
|||||

DB 380 CTGGCAAGCATACACCCCTCCAGATGCGCTCACTGCGCCTTGCAGGTGGCTGA 439
|||||

OY 2216 GCTGCTGTTGAACGGGGGCGCTCCGTCACCTCCGACCTGGAAGG 2262
|||||

DB 440 GCTGCTGTTGAACGGGGGCGCTCCGTCACCTCCGACCTGGAAGG 486
|||||

RESULT 14
BG392570 699 bp mRNA linear EST 12-MAR-2001
LOCUS BG392570
DEFINITION 602410786F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4539789 5', mRNA sequence.
IMAGE:4539789 5', mRNA sequence.
BG392570
EST.
BG392570.1 GI:13286018

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 699)
NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9abps-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: RHE I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM10468 row: K column: 22
High quality sequence stop: 578.
Location/Qualifiers
1. 699
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4539789"
/clone_lib="NIH_MGC_92"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally, oligo-dT primed. Average insert size 2.5 Kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

BASE COUNT 149 a 221 c 222 g 107 t

ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-60; Length 699;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2007 CAGGACCTTGAGGCGAGGCGCACCCCTTAACCTCGGAGACTAGTGTGACACCT 2066

Db 172 CAGGACCTTGAGGACAGGCGCACCCCTTAACCTCGGAGACTGTTGGCTGAGACACT 231
 QY 2067 CTGCACGAGGCTCGCACTAGCGGCGCATCTAGAAATTTGCCCTTCTCTGAGCACCGG 2126
 Db 232 CTGCACGAGGCTCGCACTAGCGGCGCATCTAGAAATTTGCCCTTCTCTGAGCACCGG 291
 QY 2127 GCCGAGTGGACGACCGAGTGGCCAGG 2154
 Db 292 GCCGAGTGGACGACCGAGTGGCCAGG 319

RESULT 15

AI821538

LOCUS

AI821538

DEFINITION

506 bp mRNA linear EST 24-OCT-2000

2139d01.x5 Soares ovary tumor NBH07 Homo sapiens cDNA clone

IMAGE:724705 3' similar to TR:Q13006 Q13006 I KAPPA BR. ; mRNA

sequence.

AI821538

AI821538

EST

GI:5440617

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (infoimage.llnl.gov) for further information.

This read is a RESEQUENCE of a previously sequenced human clone

Original clone citation: see original entry for original citation

Information

This 3' resequenced clone has no previous 3' data to verify this

new read against

Possible reversed clone: similarity on wrong strand

Insert length: 639 Std Error: 0.00

Seq primer: -40UP from GIBCO

High quality sequence stop: 463.

Location/Qualifiers

1. .506

/organism="Homo sapiens"

/db_xref="GDB:5936350"

/db_xref="taxon:9606"

/clone="IMAGE:724705"

/clone_id="Soares ovary tumor NBH07"

/sex="Female"

/tissue_type="ovarian tumor"

/lab_host="DH10B (ampicillin resistant)"

/note="Organ: ovary; Vector: pT773D (Pharmacia) with a

modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAAGTGGAGCGCGCGCGGTTTTTTTTTTTTTTT 3'] ,

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT773 vector

(Pharmacia). Library constructed by Bento Soares and

M.Falima Bonaldo."

M.Falima Bonaldo."

BASE COUNT

89 a 143 c 161 g 111 t 2 others

ORIGIN

Query Match

5.4%; Score 136; DB 9; Length 506;

Best Local Similarity 100.0%; Pred. NO. 1e-54;

Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2096 AGAATTTGCGCTCTGCTGAGCAGCGGCGCGAGTGGACCGGAGTGGCCAGG 2155

Db 320 AGAATTTGCGCTCTGCTGAGCAGCGGCGCGAGTGGACCGGAGTGGCCAGG 379

QY 2156 CTGCAAGGATCAGCCCGCCGACGATGGCTCAACTGTTGGCCACTTCGAGGTGGCTGA 2215
 Db 380 CTGCAAGGATCAGCCCGCCGACGATGGCTCAACTGTTGGCCACTTCGAGGTGGCTGA 439
 QY 2216 GCTGCTGCTTGAACGG 2231
 Db 440 GCTGCTGCTTGAACGG 455

Search completed: May 27, 2003, 11:56:50
 Job time : 3565 secs

